STATE OF CONNECTICUT

DEPARTMENT OF PUBLIC SAFETY
DIVISION OF STATE POLICE
FORENSIC SCIENCE LABORATORY

March 11, 1991

Dr. Victor A. McKusick
Chairman
The John Hopkins Hospital
Baltimore, MD

Dear Dr. McKusick:

Enclosed is a copy of my comments on the draft report of the committee on DNA Technology in Forensic Science which I forwarded to Oskar. If you have any questions please feel free to contact me.

With best regards,

Dr. Henry C. Lee
Director

HCL/brm

Enclosure

Phone
294 Colony Street, Meriden, CT 06450-2098

H.C. Lee: Comments on Draft Report of the Committee on DNA Technology in Forensic Science

This document is well prepared, and the format appears to be excellent for the purpose. Some of the members of the committee have clearly devoted considerable effort to the preparation of the individual chapters. I have several general comments on basic principles that it is important to include.

1. The document appears to be very critical of the forensic science community in the way it has conducted DNA testing thus far. In reality, the "forensic community" has not actually conducted very much DNA testing at all. Beginning with the reports of Alex Jeffreys and subsequent DNA testing offered by commercial enterprises (Cellmark, Lifecodes) to the more recent FBI Laboratory DNA program, all the individuals involved in the formulation of testing procedures and materials were molecular biologists, not forensic scientists. The individuals who conduct testing in those laboratories are generally molecular biologists, biochemists or technicians, and not forensic scientists. Thus, whatever can be said about DNA testing practices conducted up to now has almost nothing to do with the "forensic community" or with forensic scientists. The general impression that forensic scientists have somehow been deficient in their conduct of DNA testing procedures is not correct. This impression should not be given to readers of this document.

2. The terminology associated with "questioned" and "known" samples is inconsistent in the document. Many different terms are applied to these samples (e.g. "suspect sample," "victim sample," "evidential sample," "scene sample," "crime sample"). We should be consistent in all the chapters and not use different terms. "Questioned" and "known" samples should be sufficient to describe the nature of the specimens in most instances.

The terms "forensics" means "public debating," and has nothing whatsoever to do with forensic science in current English language usage. The term "forensic" is proper as an adjective in compound terms such as "forensic science," "forensic investigation," "forensic testing," "forensic analysis," etc. (C.2, p.2, L.7)

3. DNA typing can be performed only on biological specimens that contain nucleated cells. Not every body fluid has nucleated cells, and thus cannot be analyzed by any DNA method. Thus, use of the term "body fluid" in a number of places to indicate one kind of biological evidentiary material is not totally accurate. We should probably be very careful to say exactly what can and cannot be analyzed. This document is likely to be read by many people who will not be able to make the distinctions for themselves. (C.1, p.23, L.4)

4. Throughout the text, DNA typing is compared with fingerprint comparisons (e.g. in the genetic identity discussion, and in the data base discussion). Automated Fingerprint Identification Systems (AFIS) actually involve two data bases: a 10-print file, and a single (latent) print file. A latent print found at a crime scene can be searched for in either the 10-print or in the latent print file. An inked print record from a suspect is searched against a 10-print file for identification purposes. Thus, DNA data base searches are not the same as fingerprint file searches, and some distinctions have to be made between them. The analogy that is made in the report between the two is not quite accurate. [See, for example H.C. Lee and R.E. Gaensslen (eds.), *Advances in Fingerprint Technology*, Elsevier Forensic and Police Science Series, Elsevier Science Publishers, New York, 1991, in press; and H.C. Lee and R.E. Gaensslen, The New Technology in Latent Print Detection and Comparison, *Fingerprint and Identification Magazine* Vol. 60, No. 1: 3-9, 1987].

In addition, under current and even proposed legislation, the number of records in DNA data bases will never reach the magnitude of existing fingerprint files. I do not believe that any forensic science laboratory will check all the incoming DNA samples against the DNA profiles in the data base.; this is not the intent for setting up a national DNA data bank.

5. The analogy drawn between methods of personal identification, such as hair comparisons, traditional serological typing, fingerprints, and dental comparisons, is excellent and well presented. However, "identity" and "identification" are not the same.

We should probably introduce and use the properly forensic terms "individualization" and "partial individualization." In the discussion of traditional serological testing, it is said that "the chance of inclusion of another individual with the same markers may range from 1 in 10 to 1 in several thousand..." This is not right. First, the numbers can range from 1 in 2 (such as group O) to 1 in several hundred thousand (such as when many systems are typed and a relatively rare type is found). Second, the sentence should refer to the "frequency of occurrence of type(s) found" and not to probability or chance. (C.7, p.11)

6. In the discussion of "mixed samples" (meaning those that have contributions from more than one individual) in connection with PCR, the logic of the discussion is slightly incomplete. (C.2 & C.3)

Forensic examiners have always and will always face "mixed samples." We have no control over this. It is the nature of the work to have to analyze such specimens. Recognition of the possibility that specimens may represent mixtures, and taking this fact into account in interpretation, is the correct way to handle this problem.

We have done this for many years in traditional serological testing. [See, for example, H.C. Lee and R.E. Gaensslen, Interpretation of Serological Results, *FBI Crime Laboratory Digest* Vol. 14, No. 3: 86-94, 1987]. DNA analysis is no different. The fact that specimens may represent mixtures does not make the analytical methods for their analysis unreliable, nor the testing results incorrect.

The example given on page 10, Chpt 2, is misleading. If the results are interpreted correctly, no problems will result. In this example, we presumably have a mixture that we know is from two different people, and they have four different alleles (alleles 1,2,3 and 4). (It would be most unusual in forensic work to KNOW how many people contributed to a mixed sample; and it would be most unusual in forensic work not to have the KNOWN type of at least one of them). That aside, these results would be correctly interpreted as representing one of the following possibilities: mixture of 1/2 + 3/4; mixture of 1/3 + 2/4; mixture of 1/4 + 2/3. If the known frequencies of all possible types in the mixture were included in the interpretation, no one should be misled or misinformed. (C.2, p.10, L.4)

7. In Chapter 3 in the discussion of DNA typing data bases, it is said that "it is meaningless to say that two patterns match without providing a scientifically valid estimate (or upper bound) of the frequency with which such matches might occur by chance." This statement is not actually correct.

It is true that in cases where there is no information whatsoever about the potential origin of the questioned specimen, such information should be provided to triers of fact to give them a basis for according weight to the "match." It may not be correct to say that such a match is "meaningless." However, in a significant number of cases in which DNA typing could be used, the number of possible depositers is KNOWN to be small. For example, in a domestic disputed situation resulting in a homicide, a suspect could state that bloodstains on his clothing resulted from his own nosebleed, accidental cut, etc. In this type of situation, the only real issue would be determination of whether the bloodstain came from him or not. In such a circumstance, a match between bloodstains on the suspect's clothing and the victim's blood (assuming the victim were distinguishable) would be essentially conclusive.

8. Chapter 2, page 34, addressing the technical basis of PCR suggests that PCR is inexpensive (presumably compared with RFLP). I do not agree that PCR is inexpensive. Our experience suggests that its costs may be of the same order as RFLP (maybe more). Reagents(especially enzymes), laboratory ware, the need for extra space, etc. all contribute substantially to the cost per specimen. Probably no more labs can afford PCR than can afford RFLP.

PCR validation may not be given completely fair treatment in the report. For example, a number of forensic laboratories recently participated in the ß-site testing of Cetus' HLA-DQα typing kit. The results of this project will soon be published. Other studies involving forensic application of PCR that are relevant to validation of this methodology have been carried out in a number of laboratories. Some results have been reported at scientific meetings, and other results have been published.

9. In chapter 5, the figures on violent crime and offenders use 1983 and 1986 data. There are newer data readily available, including Uniform Crime Reports and Sourcebook of Criminal Justice Statistics for 1989.

10. The recommendations concerning certification, accreditation, proficiency testing, licensing, site inspection, oversight committees, advisory committees, etc. are all good ideas. Several important points must be kept in mind, however, if these recommendations are to achieve the purposes for which they are intended.

(a) There is significant danger that overregulation of publicly funded forensic science laboratories will effectively force them to discontinue the application of DNA in forensic cases. Costs could be so high that only commercial laboratories and a handful of large government laboratories (such as the FBI) will have sufficient personnel and funding to be able to comply with all the regulations. Having fewer laboratories which conduct DNA testing for the entire forensic community is not only

impractical (in terms of case load and case application), but also will have a detrimental effect on the application of molecular biology to the forensic science.

(b) Comparison of governmental forensic laboratories with clinical, hospital and drug testing labs is inaccurate. The latter have the ability to recover all the costs of their regulation through charges to users. Forensic laboratories have no such option. It is unlikely that governments will substantially increase the budgets of forensic laboratories on a continuing basis in order to enable them to comply and deal with too many regulations, rules, and requirements.

The end result will be that very few laboratories will offer DNA testing services. For example, the testing of urine for drugs is done almost exclusively by private concerns. Few forensic labs do such testing now, having dropped these services because of overregulation. At the same time, the quality of urine testing for drugs is still highly questionable.

(c) In this context, it seems very unwise to produce this lengthy and long-awaited report on forensic DNA testing containing recommendations for such extensive regulation, oversight, and requirements, etc., that would result in almost no forensic laboratories being able to do any DNA testing!

If the intention of the committee is to encourage the forensic science laboratories to apply DNA accurately and appropriately in forensic case work, this section should be carefully reviewed with these points in mind.